# SMGR: Setup and Introduction

*SMGR (Joint statistical method for integrative analysis of single-cell multi-omics data)*

Vignette built on April 20, 2022.

**SMGR workflow**

This tutorial goes through the steps in the SMGR workflow:

* Identify conistent signals of genes and peaks based on scRNA-seq & scATAC-seq data.
* Reveal the latent representation of co-expressed genes and peaks, i.e. co-regulatory program
* Identify co-expressed TF and target genes, based on single-cell multi-omics analysis

The setup and running steps are shown as follows in this tutorial:

**Requirements**

* Input: expression matrix The input to SMGR is a list of scRNA-seq expression matrix and scATAC-seq matrix:

*For scRNA-seq matrix:* Each column corresponds to a sample (cell) and each row corresponds to a gene. Expression units: The preferred expression values are gene-summarized raw counts. Other measurements (such as FPKM) are also accepted.

*For scATAC-seq matrix:* Each column corresponds to a sample (cell) and each row corresponds to a peak.

# Installation

The R implementation of SMGR is based on R packages as below.

Therefore, you will need to install these packages, and some extra dependencies, to run SMGR:

if (!requireNamespace("BiocManager", quietly = TRUE)) install.packages("BiocManager")  
BiocManager::version()

## [1] '3.13'

# If your bioconductor version is previous to 4.0, see the section bellow  
# Required  
packages = c('glmnet','MASS','purrr','mpath','zic','pscl','parallel')  
# BiocManager::install(packages)

Now you are ready to install SMGR:

# devtools::install\_github("QSong-github/SMGR")  
library('SMGR')

*Note: please invoke these packages to run the following codes:*

pkg = c('glmnet','MASS','purrr','mpath','zic','pscl','parallel')  
sapply(pkg, require, character.only = TRUE)

## glmnet MASS purrr mpath zic pscl parallel   
## TRUE TRUE TRUE TRUE TRUE TRUE TRUE

# Run SMGR with example data

Example data is deposited in the data folder.

# @param rna.cts simulated scRNA-seq data  
rna.cts <- readRDS('simuation\_scRNA-seq.RDS')  
  
# @param atac.cts simulated scATAC-seq data  
atac.cts <- readRDS(file='simuation\_scATAC-seq.RDS')  
  
input\_data <- list(rna.cts, atac.cts)

**SMGR process**

Input data is a list of scRNA-seq and scATAC-seq data

input\_data <- list(as.matrix(rna.cts),as.matrix(atac.cts))  
  
#result1 <- smgr\_main(sm.data = input\_data, K=nrow(input\_data[[1]]))

*if output is set to ‘all’, you will obtain the coefficients and BIC values*